

Figure 1

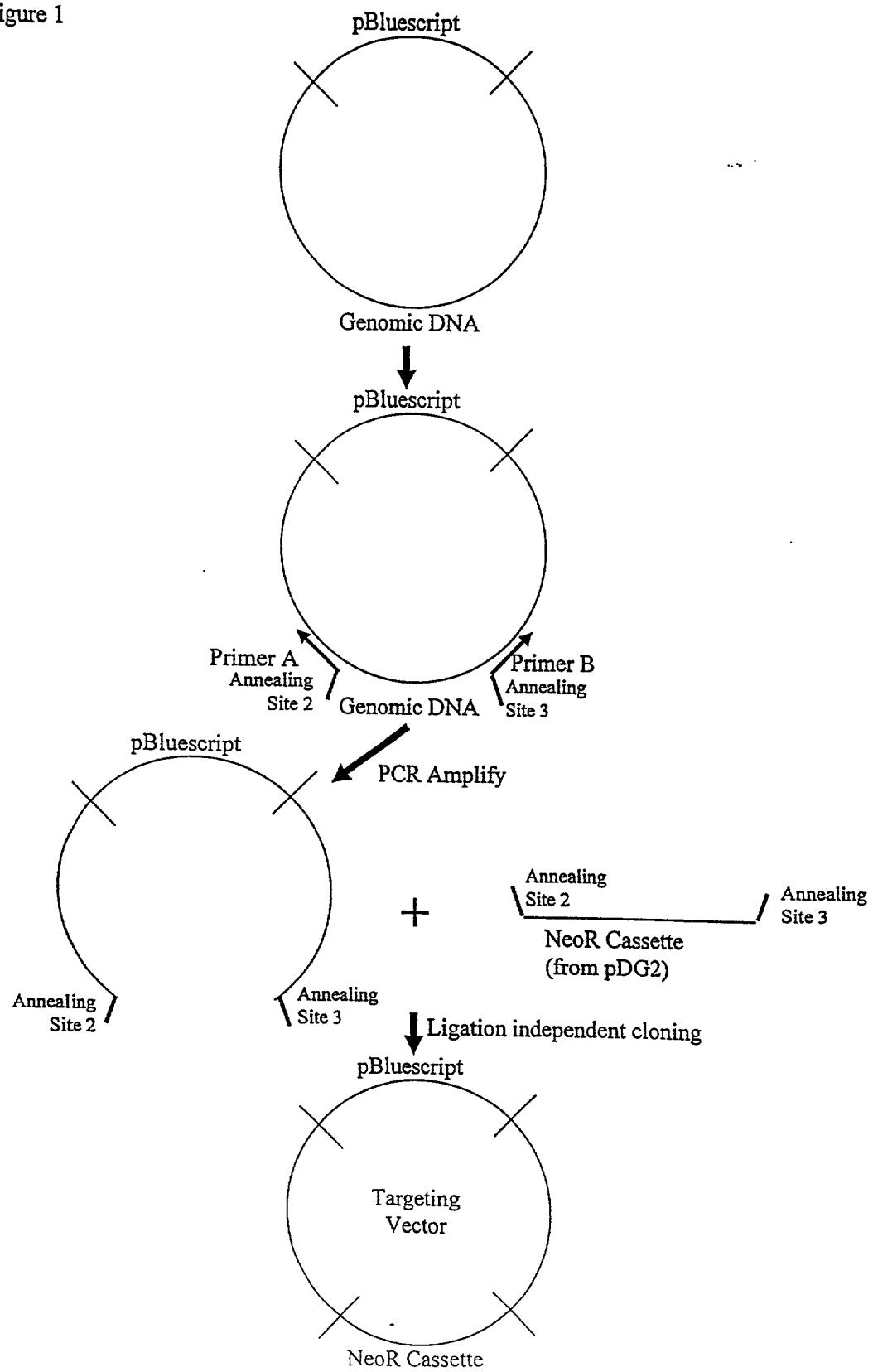
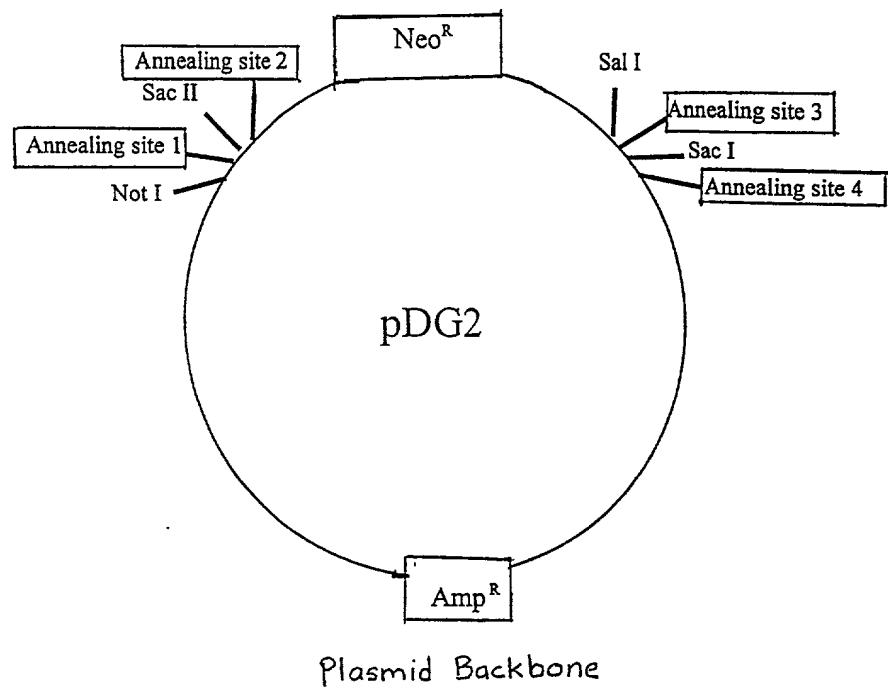


Figure 2A



pDG2:

Fig 2B

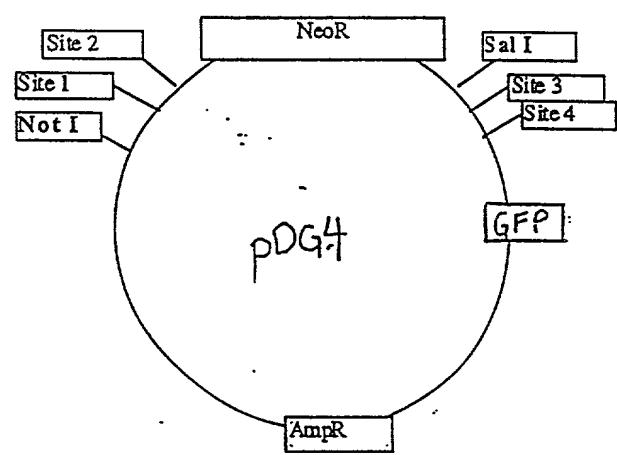


Fig 3A

pDG4:

Fig 3B

Annealing site	Sequence	Sequence after digestion
1	5' tgcgtccctttggcttgcctcaa... 3' 3' acacgaggagaaaccgaacgaagg... 5'	5' tgcgtccctttggcttgcctcaa... 3' 3' tt... 5'
2	5' ctggttcttgcgtggcttggccaa... 3' 3' gaccaagaacacagaccgaaccgg... 5'	5' ctggttcttgcgtggcttggccaa... 3' 3' tt... 5'
3	5' ggtccctcgctctgtgtccgtt... 3' 3' ccaggagcgcagacacaggcaact... 5'	5' ggtccctcgctctgtgtccgtt... 3' 3' tt... 5'
4	5' tttgcgtgtccctgtgtcgtaa... 3' 3' aaacgcacaggacacagcagct... 5'	5' tttgcgtgtccctgtgtcgtaa... 3' 3' tt... 5'

Fig 4

Annealing site	Sequence	Sequence after digestion
1	5' AAtgtgctccctttggcttgcgc 3' 3' Ttacacgaggagaaaccgaacgaagg 5'	5' AA 3' 3' Ttacacgaggagaaaccgaacgaagg 5'
2	5' AAActggttcttgcttgtggcttggccgc 3' 3' Ttgaccaagaacacagaccgaaccggg 5'	5' AA 3' 3' Ttgaccaagaacacagaccgaaccggg 5'
3	5' AAggtccctcgctctgtgtccgttGAGCT 3' 3' Ttccaggagcgagacacaggcaac 5'	5' AA 3' 3' Ttccaggagcgagacacaggcaac 5'
4	5' AAttgcgtgtccctgtgtcgctGAGCT 3' 3' Ttaaacgcacaggacacagcagc 5'	5' AA 3' 3' Ttaaacgcacaggacacagcagc 5'

Fig 5

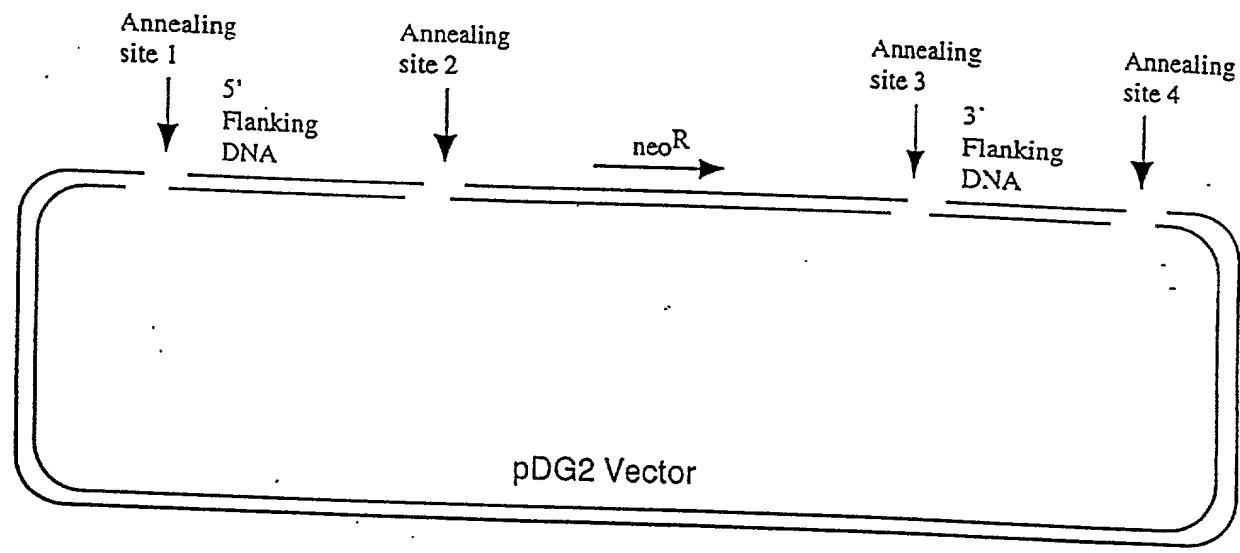


Fig 6

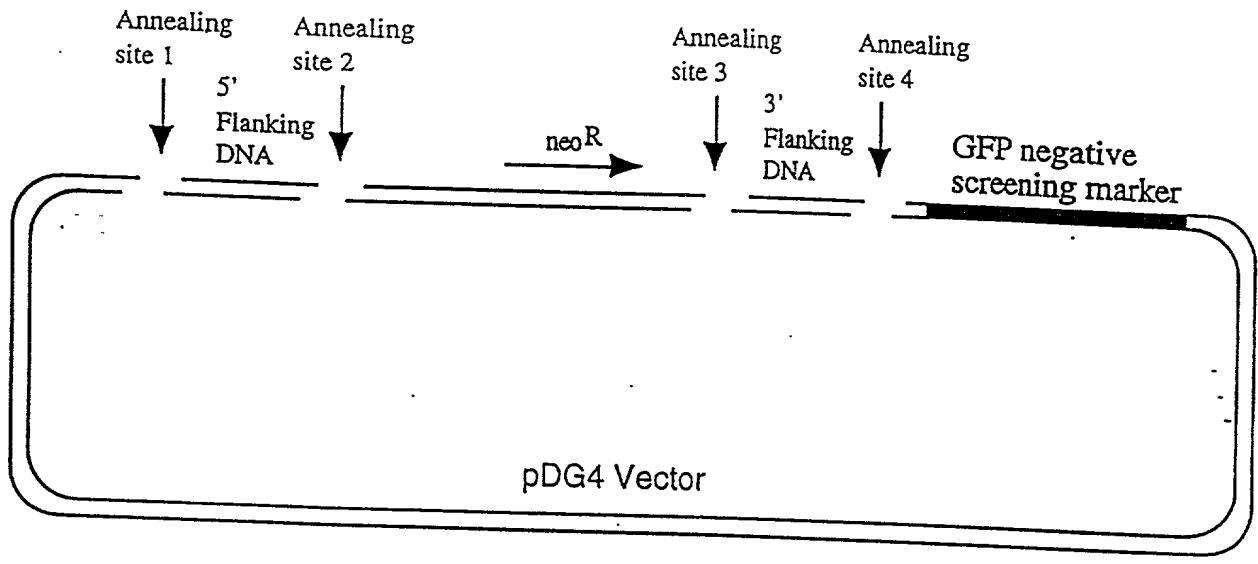


Fig 7

<u>Oligo#</u>	<u>Sequence (5' to 3')</u>
174	ATGACCGCTCAGGAAACCTGTTGCA
180	ATAGGCATAGTAGGCCAGCTTGAGG
454	tgtgctctttggcttgcgttcAATTAAACCTCACTAAAGGGAACGAAT
463	ctggttttgtctggcttggccaaTGCAACAGGTTCTGAGCGGTCA
464	ggtcctcgctctgtgtccgttgaacCCTCAAGCTGGCTACTATGCCTAT
42	tttgcgtgtctgtgtcgaaCGACTAATACGACTCACTATAAGGGCG
151	GCCAATGGACTCTTAGTTTGGAAC
155	GTTCTGGCAAACAAATTGGCGCAC
454	tgtgctctttggcttgcgttcAATTAAACCTCACTAAAGGGAACGAAT
465	ctggttttgtctggcttggccaaGTTCCAAAACTAAGAGTCCATTGGC
466	ggtcctcgctctgtgtccgttgaatGCGCCGAATTGTTGCCAGAAC
1	GAACCTTGGTGTGCCAAGTTACTTC
2	GAACTTGGCTGAACCCCTTGTCT
41	tgtgctctttggcttgcgttgaacGACTAATACGACTCACTATAAGGGCG
38	ctggttttgtctggcttggccaaGAAGTAACCTGGCACACCAAGGTT
40	ggtcctcgctctgtgtccgttgaAGAACAAAGGGTTCAGCCAAAGTTC
37	tttgcgtgtctgtgtcgAAATTAAACCTCACTAAAGGGAACGAAT
540	ATGCCGGATCTCTACTACTGGGCC
546	TGTATAGTAGACAGCGATGGAACG
445	GACAAGAACCAAGTTGACGTCAAGCTTCCGGGACGCGTGTAGCGGCGCG
667	ctggttttgtctggcttggccaaGGCCAGTAGTAGGAGATCCGGCAT
668	ggtcctcgctctgtgtccgttgaacCGTTCCATCGCTGTACTATGACA
907	ctggttttgtctggcttggccaaAAAGCCGACAGCCACGCTCACAGC
908	ggtcctcgctctgtgtccgttgaacGCCAATGCCACAGAGACAGAAATGT
1157	ctggttttgtctggcttggccaaGTTGGATCCTCTCAAGGCCCCATCT
1158	ggtcctcgctctgtgtccgttgaacCTCCAGTGCGAGTGTGGGGACAG

Figure 8